GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 10, 2004, 17:38:40 ; Search time 173 Seconds
(without alignments)
7958.573 Million cell updates/sec

Title: US-09-434-382-1
Perfect score: 2481
Sequence: 1 atgtgggcgctttgctcgct.....agaaggtcagagcccagtga 2481

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2481	100.0	2481	4	US-09-564-805-1	Sequence 1, Appli
2	2481	100.0	2958	4	US-09-564-805-3	Sequence 3, Appli
3	2455.4	99.0	2908	4	US-09-564-805-223	Sequence 223, App
4	2442.6	98.5	2892	4	US-09-564-805-225	Sequence 225, App
5	1645.6	66.3	2470	4	US-09-564-805-221	Sequence 221, App
6	734.8	29.6	783	4	US-09-833-381-2039	Sequence 2039, Ap
7	470.4	19.0	536	4	US-09-833-381-2038	Sequence 2038, Ap
8	247.4	10.0	350	4	US-09-564-805-210	Sequence 210, App
9	247.4	10.0	26664	4	US-09-564-805-28	Sequence 28, Appl
10	245	9.9	295	4	US-09-564-805-4	Sequence 4, Appli
11	237	9.6	238	3	US-09-328-111-315	Sequence 315, App
12	228	9.2	655	4	US-09-564-805-27	Sequence 27, Appl
13	145	5.8	145	4	US-09-564-805-26	Sequence 26, Appl
14	139	5.6	139	4	US-09-564-805-16	Sequence 16, Appl
15	139	5.6	139	4	US-09-564-805-20	Sequence 20, Appl
16	121	4.9	121	4	US-09-564-805-24	Sequence 24, Appl
17	120	4.8	120	4	US-09-564-805-10	Sequence 10, Appl
18	119	4.8	119	4	US-09-564-805-18	Sequence 18, Appl
19	113.6	4.6	326	4	US-09-564-805-212	Sequence 212, App
20	113	4.6	113	4	US-09-564-805-14	Sequence 14, Appl
21	110	4.4	110	4	US-09-564-805-22	Sequence 22, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2481
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2478)
US-09-564-805-1

Query Match 100.0%; Score 2481; DB 4; Length 2481;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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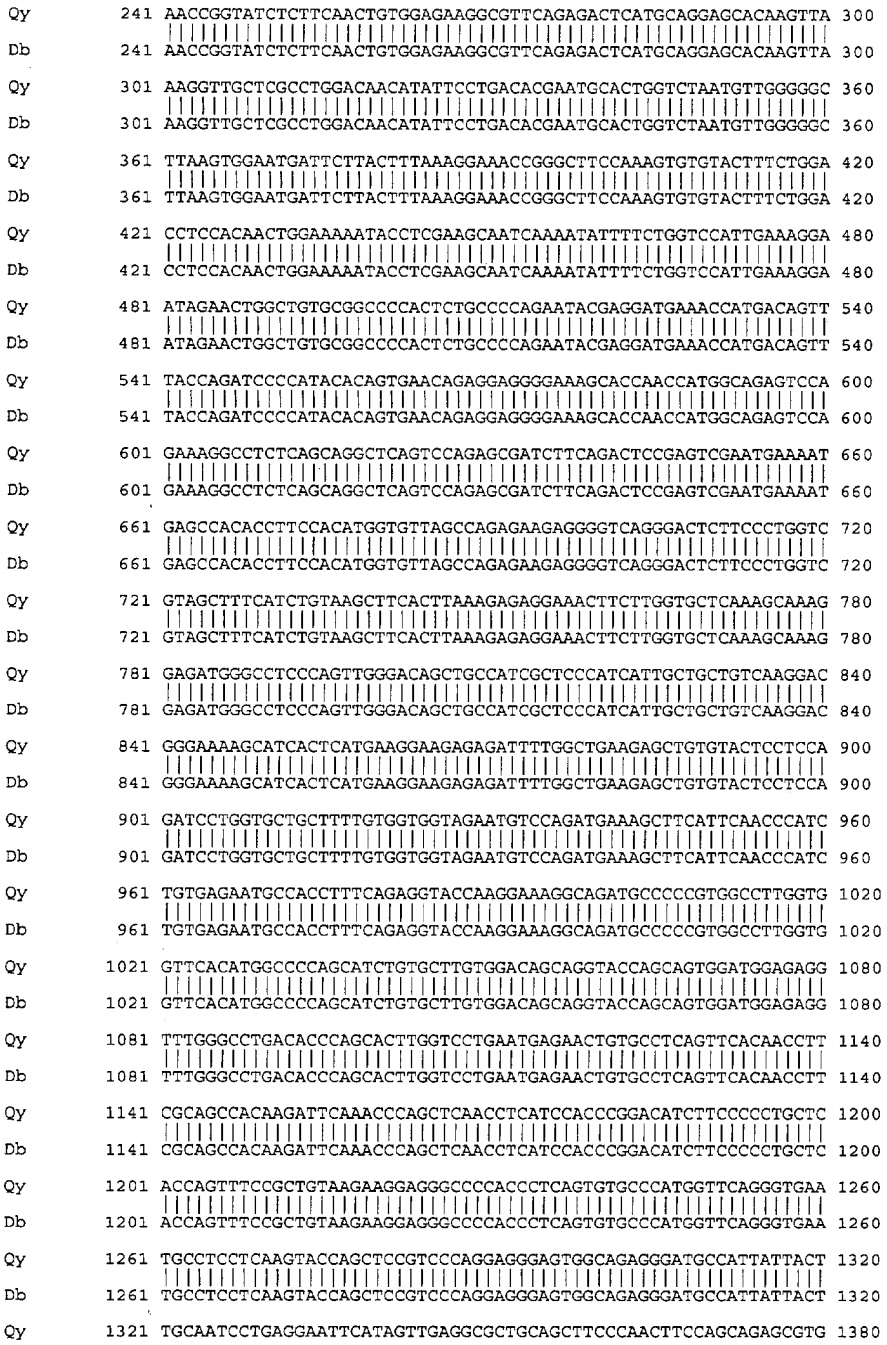
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RESULT 2
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; Sequence 3, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
;  APPLICANT:  Tavtigian, Sean V.
;  APPLICANT:  Teng, David H.F.
;  APPLICANT:  Simard, Jacques
;  APPLICANT:  Rommens, Johanna M.
;  APPLICANT:  Myriad Genetics, Inc.
;  TITLE OF INVENTION:  Chromosome 17p-Linked Prostate Cancer Susceptibility
;  TITLE OF INVENTION:  Gene and a Paralog and Orthologous Genes
;  FILE REFERENCE:  2318-258
;  CURRENT APPLICATION NUMBER: US/09/564,805
;  CURRENT FILING DATE:  2000-05-05
;  PRIOR APPLICATION NUMBER:  US 60/107,468
;  PRIOR FILING DATE:  1998-11-06
;  PRIOR APPLICATION NUMBER:  09/434,382
;  PRIOR FILING DATE:  1999-11-05
;  NUMBER OF SEQ ID NOS:  240
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 2958
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (51)..(2531)
;   OTHER INFORMATION: coding sequence as in SEQ ID NO:1
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Qy       1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1380
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Db       1371 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1430

Qy       1381 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1431 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1490

Qy       1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1491 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1550

Qy       1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1551 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1610
```

```
Qy       1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1611 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1670

Qy       1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1671 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1730

Qy       1681 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1731 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1790

Qy       1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1791 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1850

Qy       1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1851 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1910

Qy       1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1911 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1970

Qy       1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1971 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 2030

Qy       1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2031 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2090

Qy       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2091 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2150

Qy       2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2151 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2210

Qy       2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCCTCTTCAGCCCCAACTTCAGC 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2211 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCCTCTTCAGCCCCAACTTCAGC 2270

Qy       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2271 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2330

Qy       2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2331 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2390

Qy       2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2391 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2450

Qy       2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2451 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2510

Qy       2461 AAGAAGGTCAGAGCCCAGTGA 2481
             |||||||||||||||||||||
Db       2511 AAGAAGGTCAGAGCCCAGTGA 2531


RESULT 3
US-09-564-805-223
; Sequence 223, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
;  APPLICANT:  Tavtigian, Sean V.
;  APPLICANT:  Teng, David H.F.
;  APPLICANT:  Simard, Jacques
;  APPLICANT:  Rommens, Johanna M.
;  APPLICANT:  Myriad Genetics, Inc.
;  TITLE OF INVENTION:  Chromosome 17p-Linked Prostate Cancer Susceptibility
;  TITLE OF INVENTION:  Gene and a Paralog and Orthologous Genes
;  FILE REFERENCE:  2318-258
;  CURRENT APPLICATION NUMBER: US/09/564,805
;  CURRENT FILING DATE:  2000-05-05
;  PRIOR APPLICATION NUMBER:  US 60/107,468
;  PRIOR FILING DATE:  1998-11-06
;  PRIOR APPLICATION NUMBER:  09/434,382
;  PRIOR FILING DATE:  1999-11-05
;  NUMBER OF SEQ ID NOS:  240
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 223
;   LENGTH: 2908
;   TYPE: DNA
;   ORGANISM: Pan troglodytes
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2478)
US-09-564-805-223

  Query Match            99.0%;  Score 2455.4;  DB 4;  Length 2908;
  Best Local Similarity  99.4%;  Pred. No. 0;
  Matches 2465;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60

Qy         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120

Qy        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180

Qy        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240

Qy        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCATTCAGAGACTCATGCAGGAGCACAAGTTA 300

Qy        301 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360

Qy        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420

Qy        421 CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480

Qy        481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540

Qy        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 600

Qy        601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCAAATGAAAAT 660

Qy        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720
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Qy       721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780
Db       721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780

Qy       781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840
Db       781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840

Qy       841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900
Db       841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900

Qy       901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960
Db       901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960

Qy       961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020
Db       961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020

Qy      1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080
Db      1021 GTTCACATGGCCCCAGAATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080

Qy      1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140
Db      1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140

Qy      1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200
Db      1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200

Qy      1201 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260
Db      1201 ACCAGTTTCCCCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260

Qy      1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320
Db      1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320

Qy      1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1380
Db      1321 TGCAATCCTGAGGAATTCATAATTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGTGTG 1380

Qy      1381 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440
Db      1381 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440

Qy      1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500
Db      1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500

Qy      1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1560
Db      1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACG 1560

Qy      1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620
Db      1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620

Qy      1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1680
Db      1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCTAAATATCTTGCTG 1680

Qy      1681 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
Db      1681 CAGAGAGAACGAGCCTTGGCATCTTTGGGAAAGCCCTTTCACCCTTTGCTGGTGGTTGCC 1740

Qy      1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
Db      1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
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Qy      1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860
Db      1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860

Qy      1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
Db      1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920

Qy      1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980
Db      1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980

Qy      1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
Db      1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040

Qy      2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
Db      2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGACGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100

Qy      2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
Db      2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160

Qy      2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2220
Db      2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAAC 2220

Qy      2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280
Db      2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTGCAACAATG 2280

Qy      2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2340
Db      2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2340

Qy      2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400
Db      2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400

Qy      2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2460
Db      2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAACGGGCCCACACAGAGGAGCCACAGGCC 2460

Qy      2461 AAGAAGGTCAGAGCCCAGTGA 2481
Db      2461 AAGAAGGTCAGAGCCCAGTGA 2481
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RESULT 4
US-09-564-805-225
; Sequence 225, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 225
; LENGTH: 2892
; TYPE: DNA

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;   ORGANISM: Gorilla gorilla
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2478)
US-09-564-805-225

  Query Match            98.5%;  Score 2442.6;  DB 4;  Length 2892;
  Best Local Similarity  99.0%;  Pred. No. 0;
  Matches 2457;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60

Qy         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120

Qy        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGGGGCCCAAACACCGTGTACCTG 180

Qy        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240

Qy        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300

Qy        301 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAGGTTGTTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360

Qy        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420

Qy        421 CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTCCACAGCTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480

Qy        481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540

Qy        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 600
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAGGCACCAACCATGGCAGAGTCCA 600

Qy        601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660

Qy        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720

Qy        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780

Qy        781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840

Qy        841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900

Qy        901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960

Qy        961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020

Qy       1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GTTCACATGGCCCCAGAATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080

Qy       1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140

Qy       1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200

Qy       1201 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ACCAGTTTCCCCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260

Qy       1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320
              |||||||||||||||||||||||||||||||| |||||||||||||||||||| |||||
Db       1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAATGGCAGAGGGATGCCATTATCACT 1320

Qy       1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db       1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGTGTG 1380

Qy       1381 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440
              |||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||
Db       1381 CAGGAGTACAGGAGGAGTGTGCAGGACGTCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440

Qy       1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCCATGAAGATTCGAAATGTCAGT 1500

Qy       1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACG 1560

Qy       1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620

Qy       1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1680
              |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db       1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCTAAATATCTTGCTG 1680

Qy       1681 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
              |||||||||  |||||||||||||||||||| |||||||||||||||||||||||||||
Db       1681 CAGAGAGAACAAGCCTTGGCATCTTTGGGAAAGCCCCTTCACCCTTTGCTGGTGGTTGCC 1740

Qy       1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CCCAGCCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800

Qy       1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860

Qy       1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920

Qy       1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980

Qy       1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGCATGGGGAAAGATGCC 2040
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Qy       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
Db       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100

Qy       2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
Db       2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160

Qy       2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2220
Db       2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAAC 2220

Qy       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280
Db       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280

Qy       2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2340
Db       2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCCGGCGACATCGAGGAGATGGAGGAG 2340

Qy       2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400
Db       2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCGGGGAGCTGGCA 2400

Qy       2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2460
Db       2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAACGGGCCCACACAGAGGAGCCACAGGCC 2460

Qy       2461 AAGAAGGTCAGAGCCCAGTGA 2481
Db       2461 AAGAAGGTCAGAGCCCAGTGA 2481
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RESULT 5
US-09-564-805-221
; Sequence 221, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2466)
US-09-564-805-221

Query Match 66.3%; Score 1645.6; DB 4; Length 2470;
Best Local Similarity 81.6%; Pred. No. 0;
Matches 1958; Conservative 0; Mismatches 417; Indels 24; Gaps 4;

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Qy         58 CGCACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCAC 117
Db         40 CGCACCATGTCGCAGGGTTCGGCTCGTCGGCCGCGGCCACCCAAAGACCCACTGCGACAC 99

Qy        118 CTGCGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTAC 177
Db        100 CTGCGTACGCGGGAGAAGCGCGGCCC------GGGTCCCGGGGGCCCGAACACCGTGTAC 153

Qy        178 CTGCAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAG 237
Db        154 CTGCAGGTGGTGGCGGCGGGCGGCCGGGACGCGGGGGCTGCTCTCTATGTCTTCTCGGAA 213

Qy        238 TTCAACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAG 297
Db        214 TACAACAGGTACCTTTTTAACTGCGGAGAAGGCGTCCAACGACTTATGCAGGAACACAAG 273

Qy        298 TTAAAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGG 357
Db        274 ACTGAAAGTCGCTCGCTTGACAACATCTTTCTGACTCGGATGCATTGGTCAAATGTTGGG 333

Qy        358 GGCTTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCT 417
Db        334 GGGTTGTGTGGAATGATTTTAACTTTAAAGGAAACCGGGCTTCCCAAATGTGTTCTGTCT 393

Qy        418 GGACCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAA 477
Db        394 GGACCACCACAGCTGGAGAAATATCTAGAAGCAATCAAAATATTTTCTGGTCCATTGAAA 453

Qy        478 GGAATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACA 537
Db        454 GGAATAGAACTGGCCGTGCGGCCTCACTCTGCACCAGAATACAAGGATGAGACCATGACT 513

Qy        538 GTTTACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGT 597
Db        514 GTTTACCAGGTCCCTATCCACAGTGAACGGAGGTGTGGAAAGCAACAGCCATCCCAGAGC 573

Qy        598 CCAGAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAA 657
Db        574 CCCAGAACATCTCCCAACAGGCTCAGTCCCAAACAGTCATCGGACTCTGGATCAGCTGAA 633

Qy        658 AATGAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTG 717
Db        634 AATGGGC--------------AGTGCCAACAGGAAAGCATGGGGCAGGGAC-CCTCCTTA 678

Qy        718 GTCGTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCA 777
Db        679 GTGGTAGCTTTTGTCTGCAAGCTTCACTTGAGGAAAGGAAACTTCTTGGTGCTTAAAGCA 738

Qy        778 AAGGAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAG 837
Db        739 AAGGAGCTGGGCCTTCCTGTTGGGACGGCCGCCATTGCACCCATCATTGCTGCTGTCAAG 798

Qy        838 GACGGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCT 897
Db        799 GACGGGAAGAGTATCACTTACGAAGGAAGAGAGATTGCTGCTGAAGAGCTTTGTACACCC 858

Qy        898 CCAGATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCC 957
Db        859 CCAGATCCTGGTCTTGTATTCATCGTGGTAGAGTGTCCTGATGAAGGATTCATCCTGCCC 918

Qy        958 ATCTGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTG 1017
Db        919 ATCTGTGAGAACGACACCTTTAAAAGGTACCAGGCAGAGGCTGATGCACCTGTGGCGCTG 978

Qy       1018 GTGGTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAG 1077
Db        979 GTGGTCCACATAGCCCCAGAATCTGTACTCATCGACAGCAGATACCAGCAGTGGATGGAG 1038

Qy       1078 AGGTTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAAC 1137
Db        1039 AGGTTCGGGCCTGACACACAGCACCTGATTCTGAATGAGAATTGCCCCTCGGTCCACAAC 1098

Qy       1138 CTTCGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTG 1197
Db        1099 CTGCGCAGCCACAAGATTCAGACCCAGCTCAGCCTCATCCACCCTGACATCTTCCCCCAG 1158

Qy       1198 CTCACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGT 1257
Db        1159 CTTACCAGCTTCTATAGTAAGGAGGAAGGGTCCACCCTCAGCGTGCCAACAGTTCGGGGT 1218
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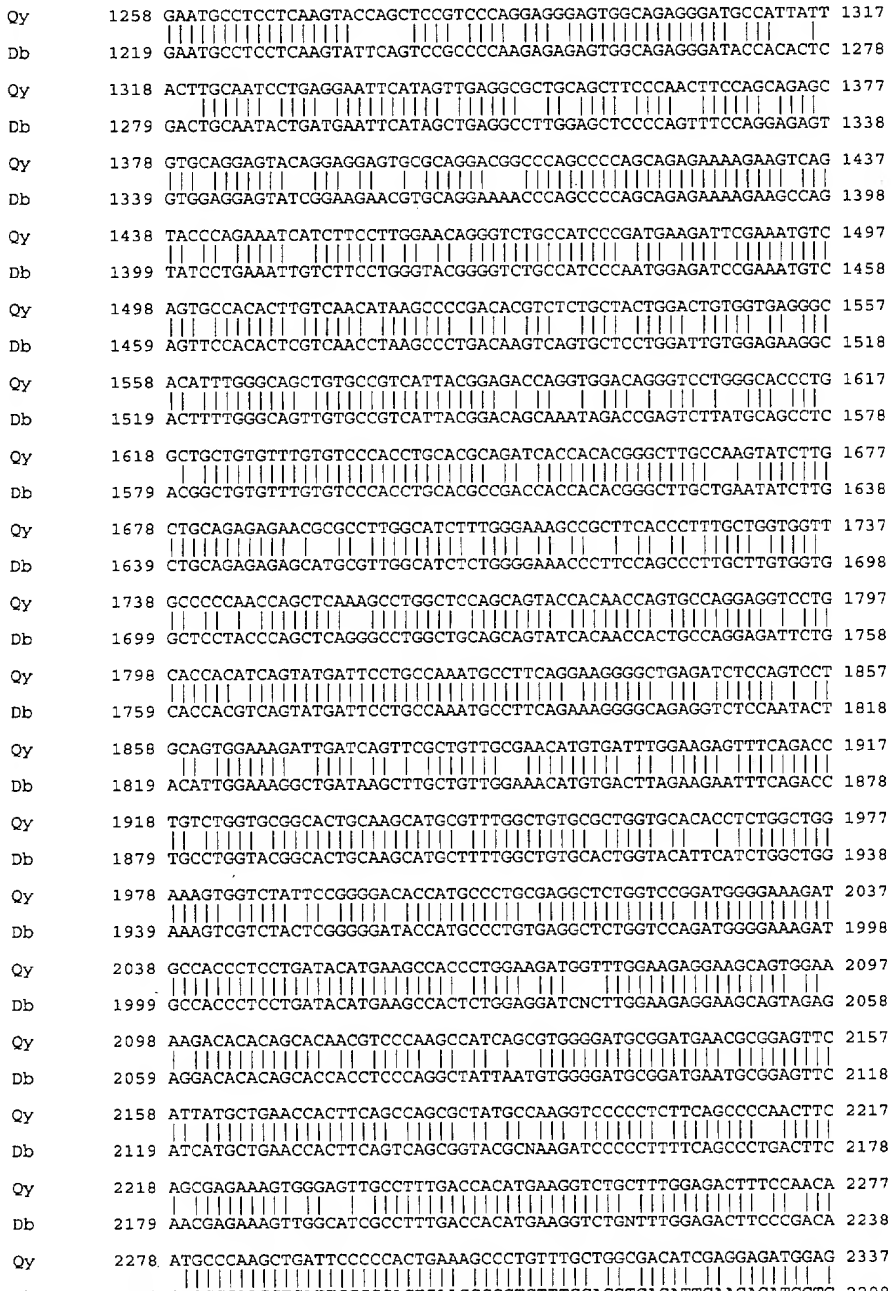
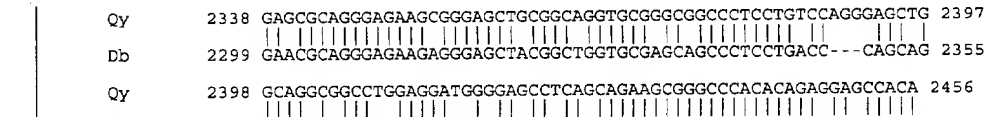
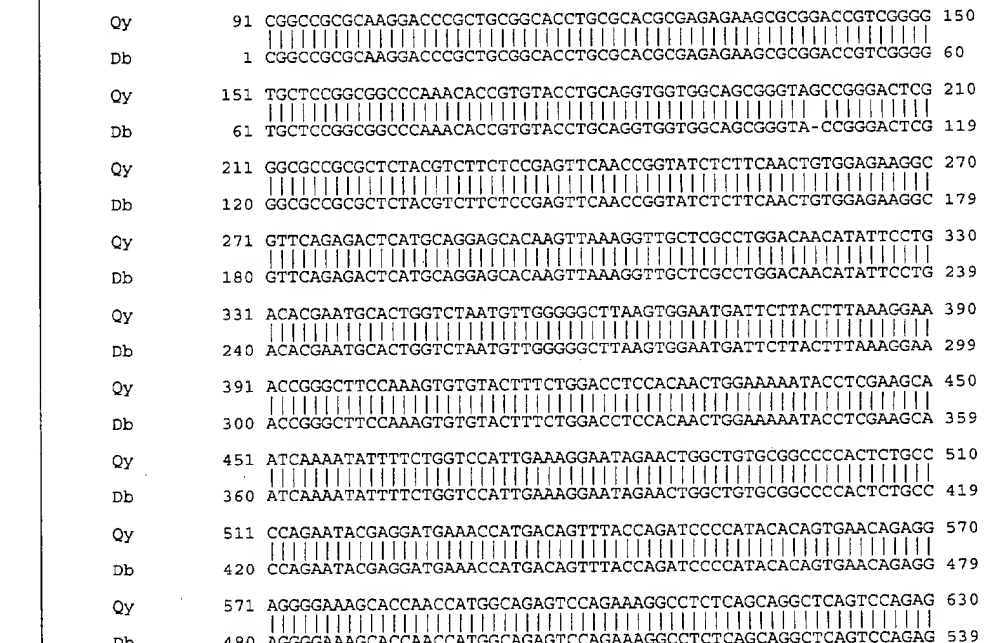




RESULT 6
US-09-833-381-2039
; Sequence 2039, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2039
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(783)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-2039

Query Match 29.6%; Score 734.8; DB 4; Length 783;
Best Local Similarity 98.3%; Pred. No. 1.3e-190;
Matches 772; Conservative 0; Mismatches 10; Indels 3; Gaps 3;



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Qy        631 CGATCTTCAGACTCCGAG-TCGAATGAAAATGAGCCACACCTTCCACATGGTGTTAGCCA 689
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        540 CGATCTTCAGACTCCGAGTTCGAATGAAAATGAGCCACACCTTCCACATGGTGTTAGCCA 599

Qy        690 GAGAAGAGGGGTCAGGGACTCTTCCCTGGTCGTAGCTTTCATCTGTAAGCTTCACTTAAA 749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 GAGAAGAGGGGTCAGGGACTCTTCCCTGGTCGTAGCTTTCATCTGTAAGCTTCACTTAAA 659

Qy        750 GAGAGGAAACTTCTTGGTGCTCAAAGCAAAGGAGATGGGCCTCCCAGTTGGGACAGCTGC 809
              |||||||||||||||||||||||||||||||||||||||||||| |||||| | ||||
Db        660 GAGAGGAAACTTCTTGGTGCTCAAAGCAAAGGAGATGGGCCTCCCATTTGGGA-AACTGC 718

Qy        810 CATCGCTCCCATCATTGCTGCTGTCAAGGACGGGAAAAGCATCACTCATGAAGGAAGAGA 869
              |||| |||||||||||||||||||||||| | |||| || ||| ||| ||||||| |||
Db        719 CATCNCTCCCATCATTGCTGCTGTCAAGGACNGNAAAACCACCACCCATAAAGGAAAAGA 778

Qy        870 GATTT 874
              |||||
Db        779 GATTT 783
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RESULT 7
US-09-833-381-2038
; Sequence 2038, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2038
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-2038

Query Match 19.0%; Score 470.4; DB 4; Length 536;
Best Local Similarity 99.8%; Pred. No. 1.5e-118;
Matches 471; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         91 CGGCCGCGCAAGGACCCGCTGCGGCACCTGCGCACGCGAGAGAAGCGCGGACCGTCGGGG 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGGCCGCGCAAGGACCCGCTGCGGCACCTGCGCACGCGAGAGAAGCGCGGACCGTCGGGG 60

Qy        151 TGCTCCGGCGGCCCAAACACCGTGTACCTGCAGGTGGTGGCAGCGGGTAGCCGGGACTCG 210
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         61 TGCTCCGGCGGCCCAAACACCGTGTACCTGCAGGTGGTTGCAGCGGGTAGCCGGGACTCG 120

Qy        211 GGCGCCGCGCTCTACGTCTTCTCCGAGTTCAACCGGTATCTCTTCAACTGTGGAGAAGGC 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCGCCGCGCTCTACGTCTTCTCCGAGTTCAACCGGTATCTCTTCAACTGTGGAGAAGGC 180

Qy        271 GTTCAGAGACTCATGCAGGAGCACAAGTTAAAGGTTGCTCGCCTGGACAACATATTCCTG 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTTCAGAGACTCATGCAGGAGCACAAGTTAAAGGTTGCTCGCCTGGACAACATATTCCTG 240

Qy        331 ACACGAATGCACTGGTCTAATGTTGGGGGCTTAAGTGGAATGATTCTTACTTTAAAGGAA 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACACGAATGCACTGGTCTAATGTTGGGGGCTTAAGTGGAATGATTCTTACTTTAAAGGAA 300

Qy        391 ACCGGGCTTCCAAAGTGTGTACTTTCTGGACCTCCACAACTGGAAAAATACCTCGAAGCA 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCGGGCTTCCAAAGTGTGTACTTTCTGGACCTCCACAACTGGAAAAATACCTCGAAGCA 360

Qy        451 ATCAAAATATTTTCTGGTCCATTGAAAGGAATAGAACTGGCTGTGCGGCCCCACTCTGCC 510
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Db        361 ATCAAAATATTTTCTGGTCCATTGAAAGGAATAGAACTGGCTGTGCGGCCCCACTCTGCC 420

Qy        511 CCAGAATACGAGGATGAAACCATGACAGTTTACCAGATCCCCATACACAGTG 562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCAGAATACGAGGATGAAACCATGACAGTTTACCAGATCCCCATACACAGTG 472
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RESULT 8
US-09-564-805-210
; Sequence 210, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (51)..(293)
US-09-564-805-210

Query Match 10.0%; Score 247.4; DB 4; Length 350;
Best Local Similarity 97.7%; Pred. No. 8.3e-58;
Matches 251; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60
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Db         51 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 110

Qy         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 170

Qy        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 230

Qy        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 290

Qy        241 AACCGGTATCTCTTCAA 257
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Db        291 AACCGGTCAGTCAACGA 307
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RESULT 9
US-09-564-805-28
; Sequence 28, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258

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;  CURRENT APPLICATION NUMBER: US/09/564,805
;  CURRENT FILING DATE:  2000-05-05
;  PRIOR APPLICATION NUMBER:  US 60/107,468
;  PRIOR FILING DATE:  1998-11-06
;  PRIOR APPLICATION NUMBER:  09/434,382
;  PRIOR FILING DATE:  1999-11-05
;  NUMBER OF SEQ ID NOS:  240
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 28
;   LENGTH: 26664
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (910)..(13104)
;   OTHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:
;   OTHER INFORMATION: 1925-1995; exon 4: 3025-3089; exon 5: 4361-4418;
;   OTHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:
;   OTHER INFORMATION: 8186-8244; exon 9: 12878-12936; exon 10:
;   NAME/KEY: misc_feature
;   LOCATION: (13756)..(22917)
;   OTHER INFORMATION: exon 11: 13756-13868; exon 12: 15283-15378; exon
;   OTHER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15:
;   OTHER INFORMATION: 18583-18701; exon 16: 20349-20445; exon 17:
;   OTHER INFORMATION: 22172-22310; exon 18: 22879-22917
;   NAME/KEY: misc_feature
;   LOCATION: (23045)..(26452)
;   OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon
;   OTHER INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23:
;   OTHER INFORMATION: 25026-25170; exon 24: 25812-26036; polyadenylation
;   OTHER INFORMATION: signal: 26447-26452
;   NAME/KEY: variation
;   LOCATION: (826)..(23879)
;   OTHER INFORMATION: s at positions 826 and 23180 is G or C; y at
;   OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486
;   OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at
;   OTHER INFORMATION: positions 22211 and 23879 is A or G.
US-09-564-805-28

  Query Match             10.0%;  Score 247.4;  DB 4;  Length 26664;
  Best Local Similarity   97.7%;  Pred. No. 9e-57;
  Matches  251;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 969

Qy         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 1029

Qy        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 1089

Qy        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 1149

Qy        241 AACCGGTATCTCTTCAA 257
              |||||||  ||  | |
Db       1150 AACCGGTCAGTCAACGA 1166


RESULT 10
US-09-564-805-4
; Sequence 4, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
;  APPLICANT:  Tavtigian, Sean V.
;  APPLICANT:  Teng, David H.F.
;  APPLICANT:  Simard, Jacques
;  APPLICANT:  Rommens, Johanna M.
;  APPLICANT:  Myriad Genetics, Inc.
;  TITLE OF INVENTION:  Chromosome 17p-Linked Prostate Cancer Susceptibility
;  TITLE OF INVENTION:  Gene and a Paralog and Orthologous Genes
;  FILE REFERENCE:  2318-258
;  CURRENT APPLICATION NUMBER: US/09/564,805
;  CURRENT FILING DATE:  2000-05-05
;  PRIOR APPLICATION NUMBER:  US 60/107,468
;  PRIOR FILING DATE:  1998-11-06
;  PRIOR APPLICATION NUMBER:  09/434,382
;  PRIOR FILING DATE:  1999-11-05
;  NUMBER OF SEQ ID NOS:  240
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 295
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (51)..(295)
;   OTHER INFORMATION: exon 1
US-09-564-805-4

  Query Match             9.9%;  Score 245;  DB 4;  Length 295;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-57;
  Matches  245;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 110

Qy         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 170

Qy        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 230

Qy        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 290

Qy        241 AACCG 245
              |||||
Db        291 AACCG 295


RESULT 11
US-09-328-111-315
; Sequence 315, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
;  APPLICANT: Endege, Wilson O.
;  APPLICANT: Steinmann, Kathleen E.
;  APPLICANT: Astle, Jon H.
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT: Bushnell, Steven E.
;  APPLICANT: Carroll III, Eddie
;  APPLICANT: Catino, Theodore J.
;  APPLICANT: Derti, Adnan
;  APPLICANT: Ford, Donna M.
;  APPLICANT: Lewis, Marcia E.
;  APPLICANT: Monahan, John E.
;  APPLICANT: Schlegel, Robert
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS
;  FILE REFERENCE: CCD-257 (US)
;  CURRENT APPLICATION NUMBER: US/09/328,111
;  CURRENT FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: US 60/088,801
;  EARLIER FILING DATE: 1998-06-10
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID NO 315
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-111-315

Query Match 9.6%; Score 237; DB 3; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.6e-55;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        176 ACCTGCAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCG 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACCTGCAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCG 60

Qy        236 AGTTCAACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACA 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTTCAACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACA 120

Qy        296 AGTTAAAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTG 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGTTAAAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTG 180

Qy        356 GGGGCTTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTAC 412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGGGCTTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTAC 237
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RESULT 12
US-09-564-805-27
; Sequence 27, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(228)
; OTHER INFORMATION: exon 24
; NAME/KEY: polyA_signal
; LOCATION: (636)..(641)
US-09-564-805-27

Query Match 9.2%; Score 228; DB 4; Length 655;
Best Local Similarity 100.0%; Pred. No. 2.3e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2254 GTCTGCTTTGGAGACTTTCCAACAATGCCCAAGCTGATTCCCCCACTGAAAGCCCTGTTT 2313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCTGCTTTGGAGACTTTCCAACAATGCCCAAGCTGATTCCCCCACTGAAAGCCCTGTTT 60

Qy       2314 GCTGGCGACATCGAGGAGATGGAGGAGCGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGG 2373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGCGACATCGAGGAGATGGAGGAGCGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGG 120

Qy       2374 GCGGCCCTCCTGTCCAGGGAGCTGGCAGGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAG 2433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGCCCTCCTGTCCAGGGAGCTGGCAGGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAG 180

Qy       2434 CGGGCCCACACAGAGGAGCCACAGGCCAAGAAGGTCAGAGCCCAGTGA 2481
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Db        181 CGGGCCCACACAGAGGAGCCACAGGCCAAGAAGGTCAGAGCCCAGTGA 228
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RESULT 13
US-09-564-805-26
; Sequence 26, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(145)
; OTHER INFORMATION: exon 23
US-09-564-805-26

Query Match 5.8%; Score 145; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.5e-30;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2109 CACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATTATGCTGAA 2168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATTATGCTGAA 60

Qy       2169 CCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGCGAGAAAGT 2228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGCGAGAAAGT 120

Qy       2229 GGGAGTTGCCTTTGACCACATGAAG 2253
              |||||||||||||||||||||||||
Db        121 GGGAGTTGCCTTTGACCACATGAAG 145
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RESULT 14
US-09-564-805-16
; Sequence 16, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06

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;  PRIOR APPLICATION NUMBER:  09/434,382
;  PRIOR FILING DATE:  1999-11-05
;  NUMBER OF SEQ ID NOS:  240
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 139
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(139)
;   OTHER INFORMATION: exon 13
US-09-564-805-16

  Query Match             5.6%;  Score 139;  DB 4;  Length 139;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-28;
  Matches  139;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1080 GTTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCT 1139
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCT 60

Qy       1140 TCGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCT 1199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCT 120

Qy       1200 CACCAGTTTCCGCTGTAAG 1218
             ||||||||||||||||||||
Db        121 CACCAGTTTCCGCTGTAAG 139


RESULT 15
US-09-564-805-20
; Sequence 20, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
;  APPLICANT:  Tavtigian, Sean V.
;  APPLICANT:  Teng, David H.F.
;  APPLICANT:  Simard, Jacques
;  APPLICANT:  Rommens, Johanna M.
;  APPLICANT:  Myriad Genetics, Inc.
;  TITLE OF INVENTION:  Chromosome 17p-Linked Prostate Cancer Susceptibility
;  TITLE OF INVENTION:  Gene and a Paralog and Orthologous Genes
;  FILE REFERENCE:  2318-258
;  CURRENT APPLICATION NUMBER: US/09/564,805
;  CURRENT FILING DATE:  2000-05-05
;  PRIOR APPLICATION NUMBER:  US 60/107,468
;  PRIOR FILING DATE:  1998-11-06
;  PRIOR APPLICATION NUMBER:  09/434,382
;  PRIOR FILING DATE:  1999-11-05
;  NUMBER OF SEQ ID NOS:  240
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 139
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(139)
;   OTHER INFORMATION: exon 17
US-09-564-805-20

  Query Match             5.6%;  Score 139;  DB 4;  Length 139;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-28;
  Matches  139;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1521 CCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACATTTGGGCAGCTGTGCCGTCA 1580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACATTTGGGCAGCTGTGCCGTCA 60

Qy       1581 TTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCTGCTGTGTTTGTGTCCCACCT 1640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCTGCTGTGTTTGTGTCCCACCT 120

Qy       1641 GCACGCAGATCACCACACG 1659
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Db        121 GCACGCAGATCACCACACG 139


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Job time : 178 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 10, 2004, 21:01:56 ; Search time 1083 Seconds
(without alignments)
11232.401 Million cell updates/sec

Title: US-09-434-382-1
Perfect score: 2481
Sequence: 1 atgtgggcgctttgctcgct.....agaaggtcagagcccagtga 2481

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
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16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	2481	100.0	2481	10	US-09-988-687-1	Sequence 1, Appli
3	2481	100.0	2481	10	US-09-988-686-1	Sequence 1, Appli
4	2481	100.0	2958	10	US-09-988-626-3	Sequence 3, Appli
5	2481	100.0	2958	10	US-09-988-687-3	Sequence 3, Appli
6	2481	100.0	2958	10	US-09-988-686-3	Sequence 3, Appli
7	2455.4	99.0	2908	10	US-09-988-626-223	Sequence 223, App
8	2455.4	99.0	2908	10	US-09-988-687-223	Sequence 223, App
9	2455.4	99.0	2908	10	US-09-988-686-223	Sequence 223, App
10	2442.6	98.5	2892	10	US-09-988-626-225	Sequence 225, App
11	2442.6	98.5	2892	10	US-09-988-687-225	Sequence 225, App
12	2442.6	98.5	2892	10	US-09-988-686-225	Sequence 225, App
13	2349	94.7	2907	16	US-10-108-260A-282	Sequence 282, App
14	1645.6	66.3	2470	10	US-09-988-626-221	Sequence 221, App
15	1645.6	66.3	2470	10	US-09-988-687-221	Sequence 221, App
16	1645.6	66.3	2470	10	US-09-988-686-221	Sequence 221, App
17	734.8	29.6	783	9	US-09-833-381-2039	Sequence 2039, Ap
18	470.4	19.0	536	9	US-09-833-381-2038	Sequence 2038, Ap
19	432.8	17.4	554	10	US-09-918-995-8996	Sequence 8996, Ap
20	247.4	10.0	350	10	US-09-988-626-210	Sequence 210, App
21	247.4	10.0	350	10	US-09-988-687-210	Sequence 210, App
22	247.4	10.0	350	10	US-09-988-686-210	Sequence 210, App
23	247.4	10.0	26664	10	US-09-988-626-28	Sequence 28, Appl
24	247.4	10.0	26664	10	US-09-988-687-28	Sequence 28, Appl
25	247.4	10.0	26664	10	US-09-988-686-28	Sequence 28, Appl
26	245	9.9	295	10	US-09-988-626-4	Sequence 4, Appli
27	245	9.9	295	10	US-09-988-687-4	Sequence 4, Appli
28	245	9.9	295	10	US-09-988-686-4	Sequence 4, Appli
29	237	9.6	238	9	US-09-879-536-315	Sequence 315, App
30	228	9.2	655	10	US-09-988-626-27	Sequence 27, Appl
31	228	9.2	655	10	US-09-988-687-27	Sequence 27, Appl
32	228	9.2	655	10	US-09-988-686-27	Sequence 27, Appl
33	145	5.8	145	10	US-09-988-626-26	Sequence 26, Appl
34	145	5.8	145	10	US-09-988-687-26	Sequence 26, Appl
35	145	5.8	145	10	US-09-988-686-26	Sequence 26, Appl
36	139	5.6	139	10	US-09-988-626-16	Sequence 16, Appl
37	139	5.6	139	10	US-09-988-626-20	Sequence 20, Appl
38	139	5.6	139	10	US-09-988-687-16	Sequence 16, Appl
39	139	5.6	139	10	US-09-988-687-20	Sequence 20, Appl
40	139	5.6	139	10	US-09-988-686-16	Sequence 16, Appl
41	139	5.6	139	10	US-09-988-686-20	Sequence 20, Appl
42	121	4.9	121	10	US-09-988-626-24	Sequence 24, Appl
43	121	4.9	121	10	US-09-988-687-24	Sequence 24, Appl
44	121	4.9	121	10	US-09-988-686-24	Sequence 24, Appl
45	120	4.8	120	10	US-09-988-626-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-988-626-1
; Sequence 1, Application US/09988626
; Publication No. US20030044959A1
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/988,626
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2481
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2478)
US-09-988-626-1

Query Match 100.0%; Score 2481; DB 10; Length 2481;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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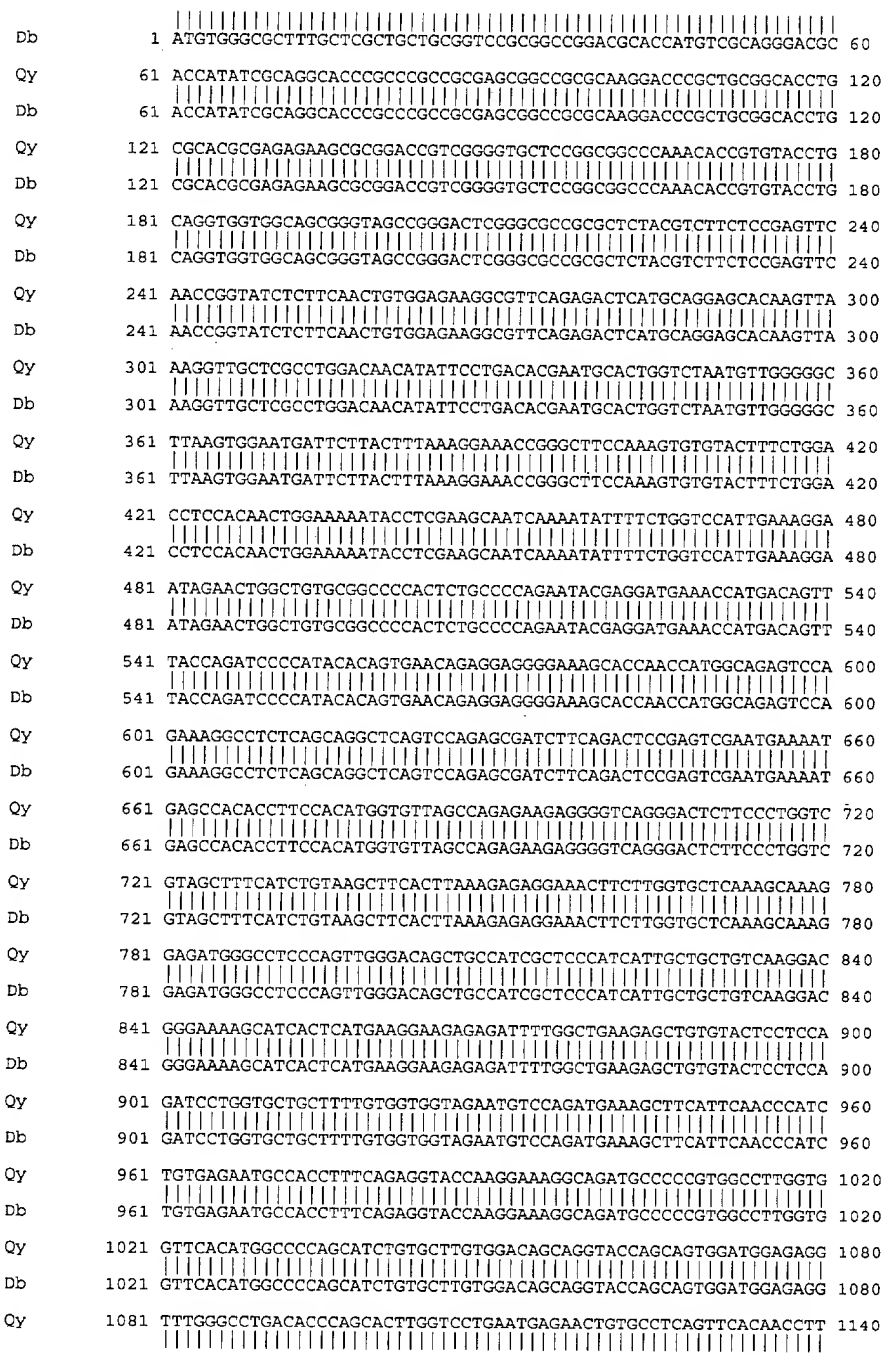
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Db 61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120
Qy 121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
Db 121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
Qy 181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240
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Db 301 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360
Qy 361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420
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Qy 421 CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480
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Qy 481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540
Db 481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540
Qy 541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 600
Db 541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 600
Qy 601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660
Db 601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660
Qy 661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720
Db 661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720
Qy 721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780
Db 721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780
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Db 841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900
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Qy 1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080
Db 1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080
Qy 1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140
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Db 1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
Qy 1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860
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Qy 1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
Db 1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
Qy 1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980
Db 1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980
Qy 1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
Db 1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
Qy 2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
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Qy 2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
Db 2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
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Db       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280

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Db       2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400

Qy       2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2460
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RESULT 2
US-09-988-687-1
; Sequence 1, Application US/09988687
; Publication No. US20030045704A1
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/988,687
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2481
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2478)
US-09-988-687-1

Query Match 100.0%; Score 2481; DB 10; Length 2481;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 600
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Qy        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720
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Db        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720

Qy        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780

Qy        781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840
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Db        781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840

Qy        841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900
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Db        841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900

Qy        901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960
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Db        901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960

Qy        961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020
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Db        961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020

Qy       1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080
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Qy       1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140
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Db       1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140

Qy       1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200
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Db       1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200

Qy       1201 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260
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Qy       1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320
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Db       1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320
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Qy       1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1380
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Qy       1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1560
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Qy       1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1680
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
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Db       1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920

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Qy       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
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Db       2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160

Qy       2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2220
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Db       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280

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RESULT 3
US-09-988-686-1
; Sequence 1, Application US/09988686
; Publication No. US20030120052A1
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/988,686
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2481
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2478)
US-09-988-686-1

Query Match 100.0%; Score 2481; DB 10; Length 2481;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60
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Db          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60

Qy         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120

Qy        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
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Db        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180

Qy        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240
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Db        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240

Qy        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300

Qy        301 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360

Qy        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420

Qy        421 CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480
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Qy        601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660
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Qy        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720
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Qy        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780
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Qy        781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840
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Qy        841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900
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Qy        901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960
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Qy       1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140
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Qy       1201 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260
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Qy       1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320
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Qy       1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500
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Db       1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1680
Qy       1681 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
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Qy       1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
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Qy       1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
Db       1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
Qy       1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980
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Qy       1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
Db       1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
Qy       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
Db       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
Qy       2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
Db       2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
Qy       2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2220
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Qy       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280
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Qy       2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2340
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Qy       2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400
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RESULT 4
US-09-988-626-3
; Sequence 3, Application US/09988626
; Publication No. US20030044959A1
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.

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;  APPLICANT:  Teng, David H.F.
;  APPLICANT:  Simard, Jacques
;  APPLICANT:  Rommens, Johanna M.
;  APPLICANT:  Myriad Genetics, Inc.
;  TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
;  TITLE OF INVENTION:  Gene and a Paralog and Orthologous Genes
;  FILE REFERENCE: 2318-258
;  CURRENT APPLICATION NUMBER: US/09/988,626
;  CURRENT FILING DATE:  2001-11-20
;  PRIOR APPLICATION NUMBER: 09/564,805
;  PRIOR FILING DATE: 2000-05-05
;  PRIOR APPLICATION NUMBER: US 60/107,468
;  PRIOR FILING DATE: 1998-11-06
;  PRIOR APPLICATION NUMBER: 09/434,382
;  PRIOR FILING DATE: 1999-11-05
;  NUMBER OF SEQ ID NOS: 240
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 2958
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (51)..(2531)
;   OTHER INFORMATION: coding sequence as in SEQ ID NO:1
US-09-988-626-3

  Query Match             100.0%;  Score 2481;  DB 10;  Length 2958;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2481;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
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Db        171 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 230

Qy        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240
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Qy        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300
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Qy        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420
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Db        411 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 470

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Db        531 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 590

Qy        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 600
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Db        591 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 650

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Db        651 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 710

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Db        711 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 770

Qy        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780
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Db        771 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 830

Qy        781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840
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Db        831 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 890

Qy        841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900
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Qy        901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960
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Db        951 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 1010

Qy        961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020
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Db       1011 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1070

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Db       1071 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1130

Qy       1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140
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Db       1131 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1190

Qy       1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200
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Db       1191 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1250

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Db       1251 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1310

Qy       1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320
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Db       1311 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1370

Qy       1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1380
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Db       1371 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1430

Qy       1381 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440
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Qy       1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500
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Db       1491 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1550

Qy       1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1560
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Qy       1681 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
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Db       1911 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1970

Qy       1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980
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Qy       1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
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Db       2031 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2090

Qy       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
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Db       2091 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2150

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Db       2151 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2210

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Db       2211 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2270

Qy       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280
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Qy       2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400
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Db       2451 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2510

Qy       2461 AAGAAGGTCAGAGCCCAGTGA 2481
             |||||||||||||||||||||
Db       2511 AAGAAGGTCAGAGCCCAGTGA 2531
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RESULT 5
US-09-988-687-3
; Sequence 3, Application US/09988687
; Publication No. US20030045704A1
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/988,687
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2958
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51)..(2531)
; OTHER INFORMATION: coding sequence as in SEQ ID NO:1
US-09-988-687-3

Query Match 100.0%; Score 2481; DB 10; Length 2958;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 110

Qy         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 170

Qy        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 230

Qy        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 290

Qy        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 350

Qy        301 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 410

Qy        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 470

Qy        421 CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 530

Qy        481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 590

Qy        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 650

Qy        601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 710

Qy        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 770

Qy        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        771 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 830

Qy        781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        831 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 890
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Qy       841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900
Db       891 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 950

Qy       901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960
Db       951 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 1010

Qy       961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020
Db      1011 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1070

Qy      1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080
Db      1071 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1130

Qy      1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140
Db      1131 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1190

Qy      1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200
Db      1191 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1250

Qy      1201 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260
Db      1251 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1310

Qy      1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320
Db      1311 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1370

Qy      1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1380
Db      1371 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1430

Qy      1381 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440
Db      1431 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1490

Qy      1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500
Db      1491 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1550

Qy      1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1560
Db      1551 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1610

Qy      1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620
Db      1611 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1670

Qy      1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1680
Db      1671 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1730

Qy      1681 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
Db      1731 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1790

Qy      1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
Db      1791 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1850

Qy      1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860
Db      1851 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1910

Qy      1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
Db      1911 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1970

Qy      1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980
Db      1971 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 2030

Qy      1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
Db      2031 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2090

Qy      2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
Db      2091 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2150

Qy      2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
Db      2151 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2210

Qy      2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2220
Db      2211 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2270

Qy      2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280
Db      2271 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2330

Qy      2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2340
Db      2331 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2390

Qy      2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400
Db      2391 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2450

Qy      2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2460
Db      2451 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2510

Qy      2461 AAGAAGGTCAGAGCCCAGTGA 2481
Db      2511 AAGAAGGTCAGAGCCCAGTGA 2531
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RESULT 6
US-09-988-686-3
; Sequence 3, Application US/09988686
; Publication No. US20030120052A1
; GENERAL INFORMATION:
;  APPLICANT: Tavtigian, Sean V.
;  APPLICANT:  Teng, David H.F.
;  APPLICANT:  Simard, Jacques
;  APPLICANT:  Rommens, Johanna M.
;  APPLICANT:  Myriad Genetics, Inc.
;  TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
;  TITLE OF INVENTION:  Gene and a Paralog and Orthologous Genes
;  FILE REFERENCE: 2318-258
;  CURRENT APPLICATION NUMBER: US/09/988,686
;  CURRENT FILING DATE:  2001-11-20
;  PRIOR APPLICATION NUMBER: 09/564,805
;  PRIOR FILING DATE: 2000-05-05
;  PRIOR APPLICATION NUMBER: US 60/107,468
;  PRIOR FILING DATE: 1998-11-06
;  PRIOR APPLICATION NUMBER: 09/434,382
;  PRIOR FILING DATE: 1999-11-05
;  NUMBER OF SEQ ID NOS: 240
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 2958
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (51)..(2531)
;   OTHER INFORMATION: coding sequence as in SEQ ID NO:1
US-09-988-686-3
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Query Match 100.0%; Score 2481; DB 10; Length 2958;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60
Db         51 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 110
Qy         61 ACCATATCGCAGGCACCCGCCCGCCGCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120
Db        111 ACCATATCGCAGGCACCCGCCCGCCGCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 170
Qy        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
Db        171 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 230
Qy        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240
Db        231 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 290
Qy        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300
Db        291 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 350
Qy        301 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360
Db        351 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 410
Qy        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420
Db        411 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 470
Qy        421 CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480
Db        471 CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 530
Qy        481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540
Db        531 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 590
Qy        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 600
Db        591 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 650
Qy        601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660
Db        651 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 710
Qy        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720
Db        711 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 770
Qy        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780
Db        771 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 830
Qy        781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840
Db        831 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 890
Qy        841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900
Db        891 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 950
Qy        901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960
Db        951 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 1010
Qy        961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020
Db       1011 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1070
Qy       1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080
Db       1071 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1130
Qy       1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140
Db       1131 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1190
Qy       1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200
Db       1191 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1250
Qy       1201 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260
Db       1251 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1310
Qy       1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320
Db       1311 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1370
Qy       1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1380
Db       1371 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1430
Qy       1381 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440
Db       1431 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1490
Qy       1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500
Db       1491 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1550
Qy       1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1560
Db       1551 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1610
Qy       1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620
Db       1611 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1670
Qy       1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1680
Db       1671 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1730
Qy       1681 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
Db       1731 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1790
Qy       1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
Db       1791 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1850
Qy       1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860
Db       1851 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1910
Qy       1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
Db       1911 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1970
Qy       1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980
Db       1971 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 2030
Qy       1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
Db       2031 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2090
Qy       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
Db       2091 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2150
Qy       2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
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Db       2151 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2210

Qy       2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2220

Db       2211 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2270

Qy       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280

Db       2271 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2330

Qy       2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2340

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Qy       2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400

Db       2391 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2450

Qy       2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2460

Db       2451 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2510

Qy       2461 AAGAAGGTCAGAGCCCAGTGA 2481

Db       2511 AAGAAGGTCAGAGCCCAGTGA 2531
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RESULT 7
US-09-988-626-223
; Sequence 223, Application US/09988626
; Publication No. US20030044959A1
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/988,626
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 223
; LENGTH: 2908
; TYPE: DNA
; ORGANISM: Pan troglodytes
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2478)
US-09-988-626-223

Query Match 99.0%; Score 2455.4; DB 10; Length 2908;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2465; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60

Db          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60

Qy         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120

Db         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120

Qy        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180

Db        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180

Qy        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240

Db        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240

Qy        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300

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RESULT 8
US-09-988-687-223
; Sequence 223, Application US/09988687
; Publication No. US20030045704A1
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/988,687
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 223
; LENGTH: 2908
; TYPE: DNA
; ORGANISM: Pan troglodytes
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2478)
US-09-988-687-223

Query Match 99.0%; Score 2455.4; DB 10; Length 2908;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2465; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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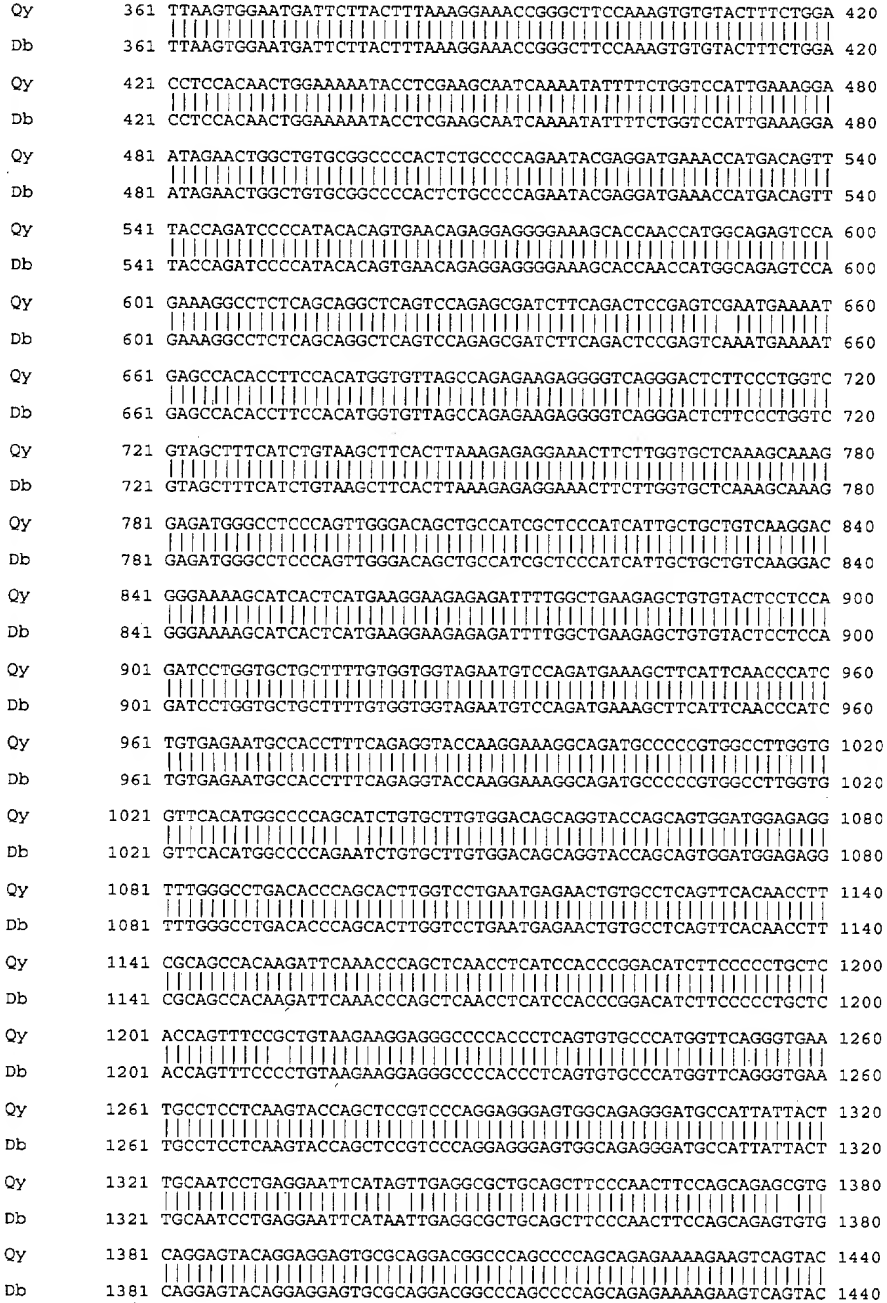
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US-09-988-686-223
; Sequence 223, Application US/09988686
; Publication No. US20030120052A1
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/988,686
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 223
; LENGTH: 2908
; TYPE: DNA
; ORGANISM: Pan troglodytes
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2478)
US-09-988-686-223

Query Match 99.0%; Score 2455.4; DB 10; Length 2908;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2465; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy        901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960
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Db        901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960

Qy        961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020

Qy       1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GTTCACATGGCCCCAGAATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080

Qy       1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140

Qy       1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200

Qy       1201 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ACCAGTTTCCCCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260

Qy       1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320

Qy       1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1380
              |||||||||||||||||||||||| ||||||||||||||||||||||||||| |||||||
Db       1321 TGCAATCCTGAGGAATTCATAATTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGTGTG 1380

Qy       1381 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440

Qy       1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500

Qy       1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACG 1560

Qy       1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620

Qy       1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1680
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Db       1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCTAAATATCTTGCTG 1680

Qy       1681 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
             |||||||||||| |||||||||||||||||||||||||  |||||||||||||||||||||||
Db       1681 CAGAGAGAACGAGCCTTGGCATCTTTGGGAAAGCCCTTTCACCCTTTGCTGGTGGTTGCC 1740

Qy       1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800

Qy       1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860

Qy       1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920

Qy       1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980

Qy       1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040

Qy       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGACGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100

Qy       2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160

Qy       2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2220
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAAC 2220

Qy       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280
             |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTGCAACAATG 2280

Qy       2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2340
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2340

Qy       2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400

Qy       2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2460
             |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAACGGGCCCACACAGAGGAGCCACAGGCC 2460

Qy       2461 AAGAAGGTCAGAGCCCAGTGA 2481
             |||||||||||||||||||||
Db       2461 AAGAAGGTCAGAGCCCAGTGA 2481


RESULT 10
US-09-988-626-225
; Sequence 225, Application US/09988626
; Publication No. US20030044959A1
; GENERAL INFORMATION:
;  APPLICANT: Tavtigian, Sean V.
;  APPLICANT:  Teng, David H.F.
;  APPLICANT:  Simard, Jacques
;  APPLICANT:  Rommens, Johanna M.
;  APPLICANT:  Myriad Genetics, Inc.
;  TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
;  TITLE OF INVENTION:  Gene and a Paralog and Orthologous Genes
;  FILE REFERENCE: 2318-258
;  CURRENT APPLICATION NUMBER: US/09/988,626
;  CURRENT FILING DATE:  2001-11-20
;  PRIOR APPLICATION NUMBER: 09/564,805
;  PRIOR FILING DATE: 2000-05-05
;  PRIOR APPLICATION NUMBER: US 60/107,468
;  PRIOR FILING DATE: 1998-11-06
;  PRIOR APPLICATION NUMBER: 09/434,382
;  PRIOR FILING DATE: 1999-11-05
;  NUMBER OF SEQ ID NOS: 240
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 225
;   LENGTH: 2892
;   TYPE: DNA
;   ORGANISM: Gorilla gorilla
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2478)
US-09-988-626-225

  Query Match            98.5%;  Score 2442.6;  DB 10;  Length 2892;
  Best Local Similarity  99.0%;  Pred. No. 0;
  Matches 2457;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60

Qy         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120

Qy        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGGGGCCCAAACACCGTGTACCTG 180

Qy        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240

Qy        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300

Qy        301 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAGGTTGTTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360

Qy        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420

Qy        421 CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTCCACAGCTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480

Qy        481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540

Qy        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 600
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAGGCACCAACCATGGCAGAGTCCA 600

Qy        601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660

Qy        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720

Qy        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780
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Qy       781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840
Db       781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840

Qy       841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900
Db       841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900

Qy       901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960
Db       901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960

Qy       961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020
Db       961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020

Qy      1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080
Db      1021 GTTCACATGGCCCCAGAATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080

Qy      1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140
Db      1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140

Qy      1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200
Db      1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200

Qy      1201 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260
Db      1201 ACCAGTTTCCCCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260

Qy      1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320
Db      1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAATGGCAGAGGGATGCCATTATCACT 1320

Qy      1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1380
Db      1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGTGTG 1380

Qy      1381 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440
Db      1381 CAGGAGTACAGGAGGAGTGTGCAGGACGTCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440

Qy      1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500
Db      1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCCATGAAGATTCGAAATGTCAGT 1500

Qy      1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1560
Db      1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACG 1560

Qy      1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620
Db      1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620

Qy      1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1680
Db      1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCTAAATATCTTGCTG 1680

Qy      1681 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
Db      1681 CAGAGAGAACAAGCCTTGGCATCTTTGGGAAAGCCCCTTCACCCTTTGCTGGTGGTTGCC 1740

Qy      1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
Db      1741 CCCAGCCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800

Qy      1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860
Db      1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860

Qy      1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
Db      1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920

Qy      1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980
Db      1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980

Qy      1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
Db      1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGCATGGGGAAAGATGCC 2040

Qy      2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
Db      2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100

Qy      2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
Db      2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160

Qy      2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2220
Db      2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAAC 2220

Qy      2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280
Db      2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280

Qy      2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2340
Db      2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCCGGCGACATCGAGGAGATGGAGGAG 2340

Qy      2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400
Db      2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCGGGGAGCTGGCA 2400

Qy      2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2460
Db      2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAACGGGCCCACACAGAGGAGCCACAGGCC 2460

Qy      2461 AAGAAGGTCAGAGCCCAGTGA 2481
Db      2461 AAGAAGGTCAGAGCCCAGTGA 2481
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RESULT 11
US-09-988-687-225
; Sequence 225, Application US/09988687
; Publication No. US20030045704A1
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/988,687
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 225
; LENGTH: 2892
; TYPE: DNA
; ORGANISM: Gorilla gorilla
; FEATURE:

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;   NAME/KEY: CDS
;   LOCATION: (1)..(2478)
US-09-988-687-225

  Query Match             98.5%;  Score 2442.6;  DB 10;  Length 2892;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 2457;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60

Qy         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120

Qy        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGGGGCCCAAACACCGTGTACCTG 180

Qy        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240
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Db        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240

Qy        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300

Qy        301 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAGGTTGTTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360

Qy        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420

Qy        421 CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTCCACAGCTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480

Qy        481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540

Qy        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 600
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAGGCACCAACCATGGCAGAGTCCA 600

Qy        601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660

Qy        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720

Qy        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780

Qy        781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840

Qy        841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900

Qy        901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960

Qy        961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020

Qy       1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GTTCACATGGCCCCAGAATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080

Qy       1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140

Qy       1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200

Qy       1201 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ACCAGTTTCCCCTGTAAGAAGGAGGGCCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260

Qy       1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320
              |||||||||||||||||||||||||||||| |||||||||||||||||||| |||||||||
Db       1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAATGGCAGAGGGATGCCATTATCACT 1320

Qy       1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1380
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGTGTG 1380

Qy       1381 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440
              |||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||
Db       1381 CAGGAGTACAGGAGGAGTGTGCAGGACGTCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440

Qy       1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCCATGAAGATTCGAAATGTCAGT 1500

Qy       1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1560
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACG 1560

Qy       1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620

Qy       1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1680
              |||||||||||||||||||||||||||||||||||||||||||||| || ||||||||||
Db       1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCTAAATATCTTGCTG 1680

Qy       1681 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
              |||||||||  |||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1681 CAGAGAGAACAAGCCTTGGCATCTTTGGGAAAGCCCCTTCACCCTTTGCTGGTGGTTGCC 1740

Qy       1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CCCAGCCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800

Qy       1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860

Qy       1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920

Qy       1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980

Qy       1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGCATGGGGAAAGATGCC 2040

Qy       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100

Qy       2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160

Qy       2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAAC 2220

Qy       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280

Qy       2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2340
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCCGGCGACATCGAGGAGATGGAGGAG 2340

Qy       2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCGGGGAGCTGGCA 2400

Qy       2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2460
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAACGGGCCCACACAGAGGAGCCACAGGCC 2460

Qy       2461 AAGAAGGTCAGAGCCCAGTGA 2481
              |||||||||||||||||||||
Db       2461 AAGAAGGTCAGAGCCCAGTGA 2481


RESULT 12
US-09-988-686-225
; Sequence 225, Application US/09988686
; Publication No. US20030120052A1
; GENERAL INFORMATION:
;  APPLICANT: Tavtigian, Sean V.
;  APPLICANT:  Teng, David H.F.
;  APPLICANT:  Simard, Jacques
;  APPLICANT:  Rommens, Johanna M.
;  APPLICANT:  Myriad Genetics, Inc.
;  TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
;  TITLE OF INVENTION:  Gene and a Paralog and Orthologous Genes
;  FILE REFERENCE: 2318-258
;  CURRENT APPLICATION NUMBER: US/09/988,686
;  CURRENT FILING DATE:  2001-11-20
;  PRIOR APPLICATION NUMBER: 09/564,805
;  PRIOR FILING DATE: 2000-05-05
;  PRIOR APPLICATION NUMBER: US 60/107,468
;  PRIOR FILING DATE: 1998-11-06
;  PRIOR APPLICATION NUMBER: 09/434,382
;  PRIOR FILING DATE: 1999-11-05
;  NUMBER OF SEQ ID NOS: 240
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 225
;   LENGTH: 2892
;   TYPE: DNA
;   ORGANISM: Gorilla gorilla
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2478)
US-09-988-686-225

  Query Match             98.5%;  Score 2442.6;  DB 10;  Length 2892;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 2457;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60

Qy         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120

Qy        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGGGGCCCAAACACCGTGTACCTG 180

Qy        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240

Qy        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300

Qy        301 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAGGTTGTTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360

Qy        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420

Qy        421 CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTCCACAGCTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480

Qy        481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540

Qy        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 600
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAGGCACCAACCATGGCAGAGTCCA 600

Qy        601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660

Qy        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720

Qy        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780

Qy        781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840

Qy        841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900

Qy        901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960

Qy        961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020

Qy       1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GTTCACATGGCCCCAGAATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080

Qy       1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140

Qy       1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200
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Qy       1201 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260
Db       1201 ACCAGTTTCCCCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260

Qy       1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320
Db       1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAATGGCAGAGGGATGCCATTATCACT 1320

Qy       1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1380
Db       1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGTGTG 1380

Qy       1381 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440
Db       1381 CAGGAGTACAGGAGGAGTGTGCAGGACGTCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440

Qy       1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500
Db       1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCCATGAAGATTCGAAATGTCAGT 1500

Qy       1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1560
Db       1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACG 1560

Qy       1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620
Db       1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620

Qy       1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1680
Db       1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCTAAATATCTTGCTG 1680

Qy       1681 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
Db       1681 CAGAGAGAACAAGCCTTGGCATCTTTGGGAAAGCCCCTTCACCCTTTGCTGGTGGTTGCC 1740

Qy       1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
Db       1741 CCCAGCCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800

Qy       1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860
Db       1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860

Qy       1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
Db       1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920

Qy       1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980
Db       1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980

Qy       1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
Db       1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGCATGGGGAAAGATGCC 2040

Qy       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
Db       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100

Qy       2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
Db       2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160

Qy       2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2220
Db       2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAAC 2220

Qy       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280
Db       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280

Qy       2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2340
Db       2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCCGGCGACATCGAGGAGATGGAGGAG 2340

Qy       2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400
Db       2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCGGGGAGCTGGCA 2400

Qy       2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2460
Db       2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAACGGGCCCACACAGAGGAGCCACAGGCC 2460

Qy       2461 AAGAAGGTCAGAGCCCAGTGA 2481
Db       2461 AAGAAGGTCAGAGCCCAGTGA 2481
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RESULT 13
US-10-108-260A-282
; Sequence 282, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 282
; LENGTH: 2907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-282

Query Match 94.7%; Score 2349; DB 16; Length 2907;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 5; Indels 57; Gaps 1;

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Qy          1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60
Db         59 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 118

Qy         61 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 120
Db        119 ACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCACCTG 178

Qy        121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 180
Db        179 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACCTG 238

Qy        181 CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC 240
Db        239 CAGGTGGTGGCAGCGGGTAGCCGGGACTCG---------------------------- 268

Qy        241 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300
Db        269 ----------------------------GGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 301

Qy        301 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360
Db        302 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 361

Qy        361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420
Db        362 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 421

Qy        421 CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480
Db        422 CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 481

Qy        481 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540
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Db        482 ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 541
Qy        541 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 TACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGTCCA 601
Qy        601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        602 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTTGAATGAAAAT 661
Qy        661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 721
Qy        721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 781
Qy        781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 841
Qy        841 GGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        842 GGGAAAAGCATCACTCATGAGGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 901
Qy        901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATC 961
Qy        961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1021
Qy       1021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAGAGG 1081
Qy       1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1141
Qy       1141 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC 1201
Qy       1201 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 ACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1261
Qy       1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACT 1321
Qy       1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1380
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1322 TGCAATCCTGAGGAACTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGCGTG 1381
Qy       1381 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAGTAC 1441
Qy       1441 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1501
Qy       1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACG 1561
Qy       1561 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 TTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1621
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Qy       1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1680
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1622 GCTGTGTTTGTGTCCCACCTGCACGCTGATCACCACACGGGCTTGCCAAGTATCTTGCTG 1681
Qy       1681 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1682 CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1741
Qy       1741 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1742 CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1801
Qy       1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1802 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1861
Qy       1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1862 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1921
Qy       1921 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1980
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1922 CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGGAAA 1981
Qy       1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1982 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2041
Qy       2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2042 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2101
Qy       2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2102 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT 2161
Qy       2161 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2162 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2221
Qy       2221 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2222 GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG 2281
Qy       2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2282 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG 2341
Qy       2341 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2400
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2342 CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 2401
Qy       2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2460
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2402 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC 2461
Qy       2461 AAGAAGGTCAGAGCCCAGTGA 2481
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Db       2462 AAGAAGGTCAGAGCCCAGTGA 2482
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RESULT 14
US-09-988-626-221
; Sequence 221, Application US/09988626
; Publication No. US20030044959A1
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

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;  TITLE OF INVENTION:  Gene and a Paralog and Orthologous Genes
;  FILE REFERENCE: 2318-258
;  CURRENT APPLICATION NUMBER: US/09/988,626
;  CURRENT FILING DATE:  2001-11-20
;  PRIOR APPLICATION NUMBER: 09/564,805
;  PRIOR FILING DATE: 2000-05-05
;  PRIOR APPLICATION NUMBER: US 60/107,468
;  PRIOR FILING DATE: 1998-11-06
;  PRIOR APPLICATION NUMBER: 09/434,382
;  PRIOR FILING DATE: 1999-11-05
;  NUMBER OF SEQ ID NOS: 240
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
;   LENGTH: 2470
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2466)
US-09-988-626-221

  Query Match             66.3%;  Score 1645.6;  DB 10;  Length 2470;
  Best Local Similarity   81.6%;  Pred. No. 0;
  Matches 1958;  Conservative    0;  Mismatches  417;  Indels   24;  Gaps    4;

Qy         58 CGCACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCAC 117
Db         40 CGCACCATGTCGCAGGGTTCGGCTCGTCGGCCGCGGCCACCCAAAGACCCACTGCGACAC 99

Qy        118 CTGCGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTAC 177
Db        100 CTGCGTACGCGGGAGAAGCGCGGCCC------GGGTCCCGGGGGCCCGAACACCGTGTAC 153

Qy        178 CTGCAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAG 237
Db        154 CTGCAGGTGGTGGCGGCGGGCGGCCGGGACGCGGGGGCTGCTCTCTATGTCTTCTCGGAA 213

Qy        238 TTCAACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAG 297
Db        214 TACAACAGGTACCTTTTTAACTGCGGAGAAGGCGTCCAACGACTTATGCAGGAACACAAG 273

Qy        298 TTAAAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGG 357
Db        274 ACTGAAAGTCGCTCGCTTGACAACATCTTTCTGACTCGGATGCATTGGTCAAATGTTGGG 333

Qy        358 GGCTTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCT 417
Db        334 GGGTTGTGTGGAATGATTTTAACTTTAAAGGAAACCGGGCTTCCCAAATGTGTTCTGTCT 393

Qy        418 GGACCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAA 477
Db        394 GGACCACCACAGCTGGAGAAATATCTAGAAGCAATCAAAATATTTTCTGGTCCATTGAAA 453

Qy        478 GGAATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACA 537
Db        454 GGAATAGAACTGGCCGTGCGGCCTCACTCTGCACCAGAATACAAGGATGAGACCATGACT 513

Qy        538 GTTTACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGT 597
Db        514 GTTTACCAGGTCCCTATCCACAGTGAACGGAGGTGTGGAAAGCAACAGCCATCCCAGAGC 573

Qy        598 CCAGAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAA 657
Db        574 CCCAGAACATCTCCCAACAGGCTCAGTCCCAAACAGTCATCGGACTCTGGATCAGCTGAA 633

Qy        658 AATGAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTG 717
Db        634 AATGGGC--------------AGTGCCAACAGGAAAGCATGGGGCAGGGAC-CCTCCTTA 678

Qy        718 GTCGTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCA 777
Db        679 GTGGTAGCTTTTGTCTGCAAGCTTCACTTGAGGAAAGGAAACTTCTTGGTGCTTAAAGCA 738

Qy        778 AAGGAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAG 837
Db        739 AAGGAGCTGGGCCTTCCTGTTGGGACGGCCGCCATTGCACCCATCATTGCTGCTGTCAAG 798

Qy        838 GACGGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCT 897
Db        799 GACGGGAAGAGTATCACTTACGAAGGAAGAGAGATTGCTGCTGAAGAGCTTTGTACACCC 858

Qy        898 CCAGATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCC 957
Db        859 CCAGATCCTGGTCTTGTATTCATCGTGGTAGAGTGTCCTGATGAAGGATTCATCCTGCCC 918

Qy        958 ATCTGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTG 1017
Db        919 ATCTGTGAGAACGACACCTTTAAAAGGTACCAGGCAGAGGCTGATGCACCTGTGGCGCTG 978

Qy       1018 GTGGTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGAG 1077
Db        979 GTGGTCCACATAGCCCCAGAATCTGTACTCATCGACAGCAGATACCAGCAGTGGATGGAG 1038

Qy       1078 AGGTTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAAC 1137
Db       1039 AGGTTCGGGCCTGACACACAGCACCTGATTCTGAATGAGAATTGCCCCTCGGTCCACAAC 1098

Qy       1138 CTTCGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTG 1197
Db       1099 CTGCGCAGCCACAAGATTCAGACCCAGCTCAGCCTCATCCACCCTGACATCTTCCCCCAG 1158

Qy       1198 CTCACCAGTTTCCGCTGTAAGAAGGAGGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGT 1257
Db       1159 CTTACCAGCTTCTATAGTAAGGAGGAAGGGTCCACCCTCAGCGTGCCAACAGTTCGGGGT 1218

Qy       1258 GAATGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATT 1317
Db       1219 GAATGCCTCCTCAAGTATTCAGTCCGCCCCAAGAGAGAGTGGCAGAGGGATACCACACTC 1278

Qy       1318 ACTTGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGC 1377
Db       1279 GACTGCAATACTGATGAATTCATAGCTGAGGCCTTGGAGCTCCCCAGTTTCCAGGAGAGT 1338

Qy       1378 GTGCAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCCCCAGCAGAGAAAAGAAGTCAG 1437
Db       1339 GTGGAGGAGTATCGGAAGAACGTGCAGGAAAACCCAGCCCCAGCAGAGAAAAGAAGCCAG 1398

Qy       1438 TACCCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTC 1497
Db       1399 TATCCTGAAATTGTCTTCCTGGGTACGGGGTCTGCCATCCCAATGGAGATCCGAAATGTC 1458

Qy       1498 AGTGCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGC 1557
Db       1459 AGTTCCACACTCGTCAACCTAAGCCCTGACAAGTCAGTGCTCCTGGATTGTGGAGAAGGC 1518

Qy       1558 ACATTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTG 1617
Db       1519 ACTTTTGGGCAGTTGTGCCGTCATTACGGACAGCAAATAGACCGAGTCTTATGCAGCCTC 1578

Qy       1618 GCTGCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTG 1677
Db       1579 ACGGCTGTGTTTGTGTCCCACCTGCACGCCGACCACCACACGGGCTTGCTGAATATCTTG 1638

Qy       1678 CTGCAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTT 1737
Db       1639 CTGCAGAGAGAGCATGCGTTGGCATCTCTGGGGAAACCCTTCCAGCCCTTGCTTGTGGTG 1698

Qy       1738 GCCCCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTG 1797
Db       1699 GCTCCTACCCAGCTCAGGGCCTGGCTGCAGCAGTATCACAACCACTGCCAGGAGATTCTG 1758

Qy       1798 CACCACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCT 1857
Db       1759 CACCACGTCAGTATGATTCCTGCCAAATGCCTTCAGAAAGGGGCAGAGGTCTCCAATACT 1818

Qy       1858 GCAGTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACC 1917
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Db       1819 ACATTGGAAAGGCTGATAAGCTTGCTGTTGGAAACATGTGACTTAGAAGAATTTCAGACC 1878

Qy       1918 TGTCTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGG 1977

Db       1879 TGCCTGGTACGGCACTGCAAGCATGCTTTTGGCTGTGCACTGGTACATTCATCTGGCTGG 1938

Qy       1978 AAAGTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGAT 2037

Db       1939 AAAGTCGTCTACTCGGGGGATACCATGCCCTGTGAGGCTCTGGTCCAGATGGGGAAAGAT 1998

Qy       2038 GCCACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAA 2097

Db       1999 GCCACCCTCCTGATACATGAAGCCACTCTGGAGGATCNCTTGGAAGAGGAAGCAGTAGAG 2058

Qy       2098 AAGACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTC 2157

Db       2059 AGGACACACAGCACCACCTCCCAGGCTATTAATGTGGGGATGCGGATGAATGCGGAGTTC 2118

Qy       2158 ATTATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTC 2217

Db       2119 ATCATGCTGAACCACTTCAGTCAGCGGTACGCNAAGATCCCCCTTTTCAGCCCTGACTTC 2178

Qy       2218 AGCGAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACA 2277

Db       2179 AACGAGAAAGTTGGCATCGCCTTTGACCACATGAAGGTCTGNTTTGGAGACTTCCCGACA 2238

Qy       2278 ATGCCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAG 2337

Db       2239 GTGCCCAAGCTGATTCCCCCACTGAAGGCCCTGTTTGCAGGTGACATTGAAGAGATGGTG 2298

Qy       2338 GAGCGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTG 2397

Db       2299 GAACGCAGGGAGAAGAGGGAGCTACGGCTGGTGCGAGCAGCCCTCCTGACC---CAGCAG 2355

Qy       2398 GCAGGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACA 2456

Db       2356 GCAGACAGCCCAGAGGACAGAGAACCCCAACAGAAGCGGGCCCACACAGATGAACCACA 2414
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RESULT 15
US-09-988-687-221
; Sequence 221, Application US/09988687
; Publication No. US20030045704A1
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/988,687
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2466)
US-09-988-687-221

Query Match 66.3%; Score 1645.6; DB 10; Length 2470;

Best Local Similarity 81.6%; Pred. No. 0;
Matches 1958; Conservative 0; Mismatches 417; Indels 24; Gaps 4;

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Qy         58 CGCACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCAAGGACCCGCTGCGGCAC 117

Db         40 CGCACCATGTCGCAGGGTTCGGCTCGTCGGCCGCGGCCACCCAAAGACCCACTGCGACAC 99

Qy        118 CTGCGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTAC 177

Db        100 CTGCGTACGCGGGAGAAGCGCGGCCC------GGGTCCCGGGGGCCCGAACACCGTGTAC 153

Qy        178 CTGCAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAG 237

Db        154 CTGCAGGTGGTGGCGGCGGGCGGCCGGGACGCGGGGGCTGCTCTCTATGTCTTCTCGGAA 213

Qy        238 TTCAACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAG 297

Db        214 TACAACAGGTACCTTTTTAACTGCGGAGAAGGCGTCCAACGACTTATGCAGGAACACAAG 273

Qy        298 TTAAAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGG 357

Db        274 ACTGAAAGTCGCTCGCTTGACAACATCTTTCTGACTCGGATGCATTGGTCAAATGTTGGG 333

Qy        358 GGCTTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCT 417

Db        334 GGGTTGTGTGGAATGATTTTAACTTTAAAGGAAACCGGGCTTCCCAAATGTGTTCTGTCT 393

Qy        418 GGACCTCCACAACTGGAAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAA 477

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Qy        478 GGAATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACA 537

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Qy        538 GTTTACCAGATCCCCATACACAGTGAACAGAGGAGGGGAAAGCACCAACCATGGCAGAGT 597

Db        514 GTTTACCAGGTCCCTATCCACAGTGAACGGAGGTGTGGAAAGCAACAGCCATCCCAGAGC 573

Qy        598 CCAGAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAA 657

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Db        634 AATGGGC--------------AGTGCCAACAGGAAAGCATGGGGCAGGGAC-CCTCCTTA 678

Qy        718 GTCGTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCA 777

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Db        799 GACGGGAAGAGTATCACTTACGAAGGAAGAGAGATTGCTGCTGAAGAGCTTTGTACACCC 858

Qy        898 CCAGATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCC 957

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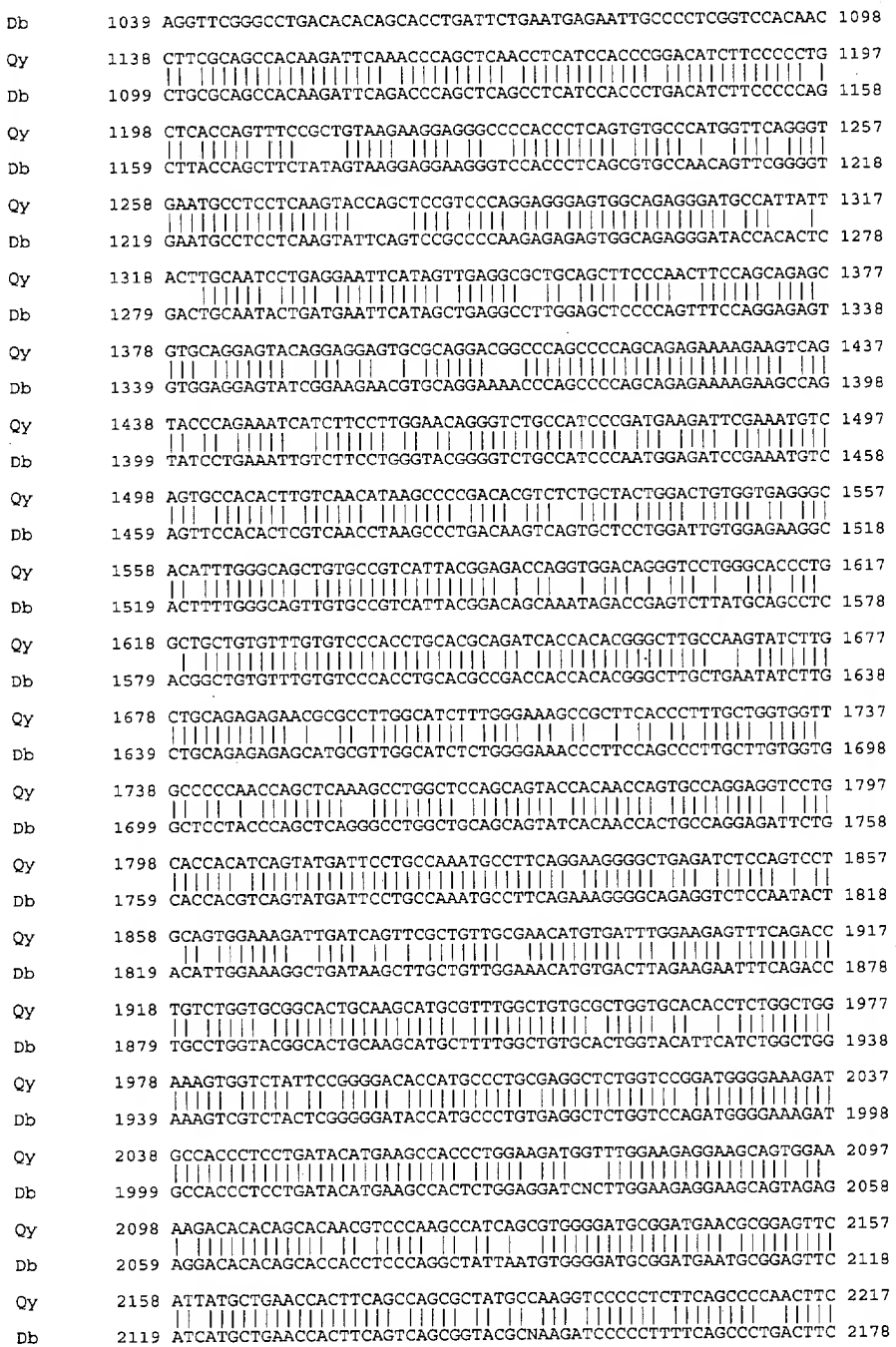

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